

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

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Application Serial Number: 10/547,532

Source: PT/10

Date Processed by STIC: 9/13/05

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Revised 01/24/05

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005
TIME: 13:24:41

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

pp 1-10

3 <110> APPLICANT: SHINTANI, ET AL.
5 <120> TITLE OF INVENTION: MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING
BRAIN/NERVE
6 CELL PROTECTIVE AGENT
8 <130> FILE REFERENCE: 20039.1USWO
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/547,532
C--> 11 <141> CURRENT FILING DATE: 2005-08-31
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002774
14 <151> PRIOR FILING DATE: 2004-03-04
16 <150> PRIOR APPLICATION NUMBER: JP 2003-056885
17 <151> PRIOR FILING DATE: 2003-03-04
19 <150> PRIOR APPLICATION NUMBER: JP 2003-106247
20 <151> PRIOR FILING DATE: 2003-04-10
22 <160> NUMBER OF SEQ ID NOS: 21
24 <170> SOFTWARE: PatentIn version 3.1

*Suggestion: Consult
sequence rules
for valid format*

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES

26 <210> SEQ ID NO: 1
27 <211> LENGTH: 288
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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32 <221> NAME/KEY: CDS
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39 <223> OTHER INFORMATION:
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E--> 48 Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Gal Leu -25
W--> 49 -20 -15 cta ctc cac ctc tgc ggc gaa tca
W--> 50 gaa gca gca agc aac ttt gac tgc 96Leu Leu His Leu Cys Gly Glu Ser Glu Ala
E--> 51 ala ser asn Phe asp cys -10 -5 -1 1
W--> 52 5 tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc
W--> 53 144Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
W--> 54 10 15 20 ttc aca cgg cag ctg

*Amend and
numbers are
completely
misaligned*

*Cumulative base
totals are at
right margin of each line.*

*Insert a
hard return.
Amino acids go directly
under their
codons.*

invalid format

RAW SEQUENCE LISTING DATE: 09/13/2005
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

same env

W--> 55 gcc aat gaa ggc tgt gac atc aat gct atc atc 192Phe Thr Arg Gln Leu Ala Asn
E--> 56 glu gly cys asp Ile asn ala Ile Ile 25 30
W--> 57 35 ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa
W--> 58 cag act 240Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
W--> 59 40 45 50 tgg gtg
W--> 60 aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg 288Trp Val Lys Tyr
E--> 61 Ile val arg Leu Leu ser Lys Lys val Lys asn met 55 60
E--> 62 65 70

83 <210> SEQ ID NO: 3
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90 <222> LOCATION: (1)..(288)
91 <223> OTHER INFORMATION:
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96 <223> OTHER INFORMATION:

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same env

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E--> 105 cys Lys his Leu Pro Phe Leu ala Leu ala gly val Leu Leu -25
E--> 106 -20 -15 -10
W--> 107 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96Ala Tyr
W--> 108 Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
W--> 109 -5 -1 1 5 ctc acg tac aca aag aac
W--> 110 gtg tat cat cat gcg aga aat ttt gtg ggt 144Leu Thr Tyr Thr Lys Asn Val Tyr
E--> 111 his his ala arg asn Phe val gly 10 15
W--> 112 20 ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct
W--> 113 atc atc 192Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
W--> 114 25 30 35 ttt cac ctg
W--> 115 aag tgc aaa aga tcc gtg tgc gct gac cca aag cag atc 240Phe His Leu Lys Ser
E--> 116 Lys arg ser val cys ala asp Pro Lys gln Ile 40 45
W--> 117 50 55 tgg gtg aaa agg att ttg cac ctc ctc agc cta aga
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E--> 119 Lys met 60 65 70

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143 <213> ORGANISM: Mus musculus
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(291)
148 <223> OTHER INFORMATION:

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Input Set : A:\PTO.AMC.txt
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150 <220> FEATURE:
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E--> 162 cys gly gly Lys arg Leu Leu Phe Leu ala Leu ala trp val -25
W--> 163 -20 -15 ctg ctg gct cac ctc tgc agc cag gca
W--> 164 gaa gca gca agc aac tac gac 96Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala
E--> 165 ala ser asn tyr asp -10 -5 -1 1
W--> 166 5 tgt tgc ctc tgc tac ata cag acg cct ctt cct tcc aga gct att gtg
W--> 167 144Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
W--> 168 10 15 20 ggt ttc aca aga cag atg
W--> 169 gcc gat gaa gct tgt gac att aat gct atc 192Gly Phe Thr Arg Gln Met Ala Asp
E--> 170 glu ala cys asp Ile asn ala Ile 25 30
W--> 171 35 atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag
W--> 172 cag 240Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
W--> 173 40 45 50 aac tgg gtg aaa
W--> 174 agg gct gtg aac ctc ctc agc cta aga gtc aag aag 288Asn Trp Val Lys Arg Ala
E--> 175 val asn Leu Leu ser Leu arg val Lys Lys 55 60
W--> 176 65 atg
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203 <213> ORGANISM: Homo sapiens
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E--> 212 gly glu ser met asn Phe ser asp val Phe asp ser ser glu 1
W--> 213 5 10 15 gat tat ttt gtg tca gtc
W--> 214 aat act tca tat tac tca gtt gat tct gag 96Asp Tyr Phe Val Ser Val Asn Thr
E--> 215 ser tyr tyr ser val asp ser glu 20 25
W--> 216 30 atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta
W--> 217 ttt 144Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
W--> 218 35 40 45 gta ccg att gcc
W--> 219 tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat 192Val Pro Ile Ala Tyr Ser
E--> 220 Leu Ile cys val Phe gly Leu Leu gly asn 50 55
W--> 221 60 att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc
W--> 222 agg tct atg 240Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser
E--> 223 met 65 70 75 80
W--> 224 aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt 288Thr Asp

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

W--> 225 Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val *same*
W--> 226 85 90 95 ctt act ctc cca ttc tgg
W--> 227 gca gtg agt cat gcc act ggt gcg tgg gtt 336Leu Thr Leu Pro Phe Trp Ala Val
E--> 228 ser his ala thr gly ala trp val 100 105
W--> 229 110 ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc
W--> 230 aac 384Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
W--> 231 115 120 125 ttt aac tgc ggg
W--> 232 atg ctg ctc ctg act tgc att agc atg gac cgg tac 432Phe Asn Cys Gly Met Leu
E--> 233 Leu Leu thr cys Ile ser met asp arg tyr 130 135
W--> 234 140 atc gcc att gta cag gcg act aag tca ttc cgg ctc cga
W--> 235 tcc aga aca 480Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg
E--> 236 thr 145 150 155 160
W--> 237 cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc 528Leu Pro
W--> 238 Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
W--> 239 165 170 175 atc atc tcc agc tca act
W--> 240 ttt gtc ttc aac caa aaa tac aac acc caa 576Ile Ile Ser Ser Ser Thr Phe Val
E--> 241 Phe asn gln Lys tyr asn thr gln 180 185
W--> 242 190 ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tgc gag ccc
W--> 243 atc 624Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
W--> 244 195 200 205 agg tgg aag ctg
W--> 245 ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt 672Arg Trp Lys Leu Leu Met
E--> 246 Leu gly Leu glu Leu Leu Phe gly Phe Phe 210 215
W--> 247 220 atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att
W--> 248 gtc aaa acc 720Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys
E--> 249 thr 225 230 235 240
W--> 250 ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc 768Leu Val
W--> 251 Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
W--> 252 245 250 255 ata gct gtg gtg ctt gtg
W--> 253 ttt ctg gct tgt cag att cct cat aac atg 816Ile Ala Val Val Leu Val Phe Leu
E--> 254 ala cys gln Ile Pro his asn met 260 265
W--> 255 270 gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc
W--> 256 tgc 864Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
W--> 257 275 280 285 cag agc gaa aag
W--> 258 cta att ggc tat acg aaa act gtc aca gaa gtc ctg 912Gln Ser Glu Lys Leu Ile
E--> 259 gly tyr thr Lys thr val thr glu val Leu 290 295
W--> 260 300 gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct
W--> 261 ttt att ggg 960Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile
E--> 262 gly 305 310 315 320
W--> 263 cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt 1008Gln Lys
W--> 264 Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
W--> 265 325 330 335 gtg aga agg aag tac aag
W--> 266 tcc tca ggc ttc tcc tgt gcc ggg agg tac 1056Val Arg Arg Lys Tyr Lys Ser Ser
E--> 267 gly Phe ser cys ala gly arg tyr 340 345
W--> 268 350 tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac
W--> 269 aat 1104Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
W--> 270 355 360 365 gcg tgc tcc ttc
W--> 271 act atg 1122Ala Ser Ser Phe Thr Met
E--> 272 370

329 <210> SEQ ID NO: 9

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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

330 <211> LENGTH: 1101
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332 <213> ORGANISM: Mus musculus
334 <220> FEATURE:
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336 <222> LOCATION: (1)..(1101)
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W--> 339 <400> 9
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W--> 342 5 10 15 gag tat tat tct att cct
W--> 343 cca gac cat ggg cca tgc tcc cta gaa gag 96Glu Tyr Tyr Ser Ile Pro Pro Asp
E--> 344 his gly Pro cys ser Leu glu glu 20 25
W--> 345 30 gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta
W--> 346 ata 144Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
W--> 347 35 40 45 tgt gtc ttt ggc
W--> 348 ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc 192Cys Val Phe Gly Leu Leu
E--> 349 gly asn Ile met val val met thr Phe ala 50 55
W--> 350 60 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg
W--> 351 ttg aac atg 240Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
E--> 352 met 65 70 75 80
W--> 353 gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288Ala Ile
W--> 354 Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
W--> 355 85 90 95 act cat gcc acc aac act
W--> 356 tgg gtt ttc agc gat gca ctg tgt aaa ctg 336Thr His Ala Thr Asn Thr Trp Val
E--> 357 Phe ser asp ala Leu cys Lys Leu 100 105
W--> 358 110 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc
W--> 359 ctg 384Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
W--> 360 115 120 125 gcc tgt atc agc
W--> 361 atg gac cgg tac att gcc atc gtc cag gca acc aaa 432Ala Cys Ile Ser Met Asp
E--> 362 arg tyr Ile ala Ile val gln ala thr Lys 130 135
W--> 363 140 tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag
W--> 364 gtc atc tgt 480Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile
E--> 365 cys 145 150 155 160
W--> 366 gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc 528Val Ala
W--> 367 Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
W--> 368 165 170 175 ttc aac aag aaa tac gag
W--> 369 ctg cag gat cgt gat gtc tgt gag cca cgg 576Phe Asn Lys Lys Tyr Glu Leu Gln
E--> 370 asp arg asp val cys glu Pro arg 180 185
W--> 371 190 tac agg tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg
W--> 372 gga 624Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
W--> 373 195 200 205 ctg gag ctg ttc
W--> 374 ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc 672Leu Glu Leu Phe Phe Gly
E--> 375 Phe Phe thr Pro Leu Leu Phe met val Phe 210 215
W--> 376 220 tgc tat ctg ttc att atc aag acc ttg gtg cag gcc cag
W--> 377 aac tcc aag 720Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser
E--> 378 Lys 225 230 235 240
W--> 379 agg cac aga gcc atc cga gtc gtg atc gct gtg gtt ctc gtg ttc ctg 768Arg His
W--> 380 Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu

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Input Set : A:\PTO.AMC.txt
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W--> 381 245          250          255          get tgt cag atc cct cac
W--> 382 aac atg gtc ctc ctc gtg act gcg gtc aac      816Ala Cys Gln Ile Pro His Asn Met
E--> 383 val Leu Leu val thr ala val asn          260          265
W--> 384 270          acg ggc aaa gtg ggc cgg agc tgc agc acc gag aaa gtc ctc gcc
W--> 385 tac      864Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
W--> 386 275          280          285          acc agg aac gtg
W--> 387 gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac      912Thr Arg Asn Val Ala Glu
E--> 388 val Leu ala Phe Leu his cys cys Leu asn          290          295
W--> 389 300          ccc gtg ttg tat gcg ttt att gga cag aaa ttc aga aac
W--> 390 tac ttc atg      960Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe
E--> 391 met          305          310          315          320
W--> 392 aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct      1008Lys Ile
W--> 393 Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
W--> 394 325          330          335          ggc ttc ctc tgt gcc cgg
W--> 395 gtt tac tcg gaa agc tac atc tcc agg cag      1056Gly Phe Leu Cys Ala Arg Val Tyr
E--> 396 ser glu ser tyr Ile ser arg gln          340          345
W--> 397 350          acc agt gag acc gtc gaa aat gat aat gca tcg tcc ttt acc atg
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E--> 399 355          360          365

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487 <222> LOCATION: (343)..(1443)
488 <223> OTHER INFORMATION:

*Cumulative base
totals are at right
margin of each line*

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W--> 492 60acacactgc ttgaagagt ccagcccca gcagaactgc aagggcagac actgttctgg
W--> 493 120ccactgcag ttgaagtca tcactttcaa tccccctgtg actagggcca gggtcttcac
W--> 494 180acctgcgaga ggaagcaaag atctaagcaa tctgaatttt aagagagaaa ctgcagctgt
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E--> 496 300ctggccagcc cacttcggag ctcagcgttt ccttgggaaa cg atg aat ttc acc      354
E--> 497 met asn Phe thr          1
W--> 498 gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg      402Glu Ala
E--> 499 asn tyr gly met glu asp tyr thr gly ser asp tyr ser met          5
W--> 500 10          15          20          ttt cca gag acc gag cca tgc
W--> 501 tct ctg caa gag gtc aga gac ttc acc      450Phe Pro Glu Thr Glu Pro Cys Ser Leu
E--> 502 gln glu val arg asp Phe thr          25          30
W--> 503 35          aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc
W--> 504 498Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu
W--> 505 40          45          50          ctt ggc aat att atg
W--> 506 gtg gtg ata acc ttt gcc ttc tac aag aaa gcc      546Leu Gly Asn Ile Met Val Val
E--> 507 Ile thr Phe ala Phe tyr Lys Lys ala          55          60
W--> 508 65          agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca
W--> 509 gac ata      594Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
W--> 510 70          75          80          ctc ttt gtc
W--> 511 ctc acc cta cca ttc tgg gca gtt act cat gcc act gac      642Leu Phe Val Leu Thr

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Input Set : A:\PTO.AMC.txt
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same

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E--> 512 Leu Pro Phe trp ala val thr his ala thr asp      85          90
W--> 513 95          100          act tgg atc ttt ggc aac acg atg tgt aaa ctg atg
W--> 514 aaa ggc acg tat      690Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly
E--> 515 thr tyr          105          110          115
W--> 516 gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg      738Ala Val
E--> 517 asn Phe asn cys gly met Leu Leu Leu ala cys ile ser met          120
W--> 518 125          130          gac cgg tac att gcc atc gtc cag gcg acc
W--> 519 aaa tct ttc cgg gta cgc      786Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
E--> 520 Phe arg val arg          135          140          145
W--> 521 tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc      834Ser Arg
E--> 522 thr Leu thr his ser Lys val ile cys Leu thr val trp Phe          150
W--> 523 155          160          gtt tcc atc atc atc tca agc ccc
W--> 524 aca ttc ttc ttc aac aag caa tac      882Val Ser Ile Ile Ile Ser Ser Pro Thr Phe
E--> 525 Phe Phe asn Lys gln tyr          165          170          175
W--> 526 180          aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tgc
W--> 527 930Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser
W--> 528 185          190          195          gag ccc atc acg tgg aaa
W--> 529 ctg ctg ggc atg gga ctc gag ctg ctc ttt      978Glu Pro Ile Thr Trp Lys Leu Leu
E--> 530 gly met gly Leu glu Leu Leu Phe          200          205
W--> 531 210          ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc
W--> 532 atc      1026Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile
W--> 533 215          220          225          atc aag acc ttg
W--> 534 gtg cag gcc cag aat tcc aag agg cac aga gcc atc      1074Ile Lys Thr Leu Val Gln
E--> 535 ala gln asn ser Lys arg his arg ala ile          230          235
W--> 536 240          cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt
W--> 537 cag atc cct      1122Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile
E--> 538 Pro          245          250          255          260
W--> 539 cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc      1170His Asn
W--> 540 Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly
W--> 541 265          270          275          cgc agc tgc agc gcc gag
W--> 542 aaa gcc ctc gcc tac gcc agg aat gtg gct      1218Arg Ser Cys Ser Ala Glu Lys Ala
E--> 543 Leu ala tyr ala arg asn val ala          280          285
W--> 544 290          gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat
W--> 545 gcc      1266Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala
W--> 546 295          300          305          ttc att gga cag
W--> 547 aaa ttc aga agc tac ttc atg aag atc atg aag gat      1314Phe Ile Gly Gln Lys Phe
E--> 548 arg ser tyr Phe met Lys Ile met Lys asp          310          315
W--> 549 320          gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc
W--> 550 ttc tgt gcc      1362Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys
E--> 551 ala          325          330          335          340
W--> 552 cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta      1410Arg Val
W--> 553 Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val
W--> 554 345          350          355          gaa aat gac aac gca tcg
W--> 555 tcc ttt acc atg taa cacgagagca caaagcagca      1463Glu Asn Asp Asn Ala Ser Ser Phe
E--> 556 thr met          360          365
E--> 557 tgccccgaaa gcctttgtga aacttgctat tacatgtga          1502
612 <210> SEQ ID NO: 15
613 <211> LENGTH: 1309
614 <212> TYPE: DNA

```


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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

615 <213> ORGANISM: Rattus norvegicus (liver)
617 <220> FEATURE:
618 <221> NAME/KEY: CDS
619 <222> LOCATION: (150)..(1250)
620 <223> OTHER INFORMATION:

same

W--> 622 <400> 15
E--> 623 gcattctcact acccgctctct caatgagcac cgtgtgttgt gcctgtcaac agaatagtcc
W--> 624 60tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagccac
E--> 625 120ttcggagctc agcgtttcct tgggaaacg atg aat ttc acc gag gcc aac tac 173
E--> 626 met asn Phe thr glu ala asn tyr 1
W--> 627 5 gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca
W--> 628 gag acc 221Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr
W--> 629 10 15 20 gag cca tgc
W--> 630 tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg 269Glu Pro Cys Ser Leu
E--> 631 gln glu val arg asp Phe thr Lys val Phe val 25 30
W--> 632 35 40 cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc
W--> 633 ctt ggc aat att 317Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly
E--> 634 asn ile 45 50 55
W--> 635 atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act 365Met Val
E--> 636 val ile thr Phe ala Phe tyr Lys Lys ala arg ser met thr 60
W--> 637 65 70 gac gtc tac cta ttg aac atg gcc atc aca
W--> 638 gac ata ctc ttt gtc ctc 413Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
E--> 639 Leu Phe val Leu 75 80 85
W--> 640 acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt 461Thr Leu
E--> 641 Pro Phe trp ala val thr his ala thr asp thr trp ile Phe 90
W--> 642 95 100 ggc aac acg atg tgt aaa ctg atg
W--> 643 aaa ggc acg tat gcg gtc aac ttt 509Gly Asn Thr Met Cys Lys Leu Met Lys Gly
E--> 644 thr tyr ala val asn Phe 105 110 115
W--> 645 120 aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att
W--> 646 557Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile
W--> 647 125 130 135 gcc atc gtc cag gcg acc
W--> 648 aaa tct ttc cgg gta cgc tcc aga aca ctg 605Ala Ile Val Gln Ala Thr Lys Ser
E--> 649 Phe arg val arg ser arg thr Leu 140 145
W--> 650 150 acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc
W--> 651 atc 653Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile
W--> 652 155 160 165 atc tca agc ccc
W--> 653 aca ttc ttc ttc aac aag caa tac aag ctg cag ggc 701Ile Ser Ser Pro Thr Phe
E--> 654 Phe Phe asn Lys gln tyr Lys Leu gln gly 170 175
W--> 655 180 cgt gat gtc tgc gag cct cag tac aag ctc gtc tgc gag
W--> 656 ccc atc acg 749Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile
E--> 657 thr 185 190 195 200
W--> 658 tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc 797Trp Lys
W--> 659 Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile
W--> 660 205 210 215 cct ttg ctg ttt atg gtg
W--> 661 ttc tgt tac ctg ttc atc atc aag acc ttg 845Pro Leu Leu Phe Met Val Phe Cys
E--> 662 tyr Leu Phe Ile Ile Lys thr Leu 220 225
W--> 663 230 gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg
W--> 664 att 893Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile
W--> 665 235 240 245 gct gtg gtt ctc

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some

```
W--> 666 gtg ttc ctg gct tgt cag atc cct cac aac atg gtc      941Ala Val Val Leu Val Phe
E--> 667 Leu ala cys gln ile Pro his asn met val      250      255
W--> 668 260      ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc
W--> 669 agc tgc agc      989Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys
E--> 670 ser      265      270      275      280
W--> 671 gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct      1037Ala Glu
W--> 672 Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala
W--> 673 285      290      295      ttc ctg cac tgc tgt ctc
W--> 674 aac ccc gtg ttg tat gcc ttc att gga cag      1085Phe Leu His Cys Cys Leu Asn Pro
E--> 675 val Leu tyr ala Phe Ile gly gln      300      305
W--> 676 310      aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt
W--> 677 atg      1133Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met
W--> 678 315      320      325      agg agg aag agc
W--> 679 aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca      1181Arg Arg Lys Ser Lys Val
E--> 680 Pro thr Phe Phe cys ala arg val tyr ser      330      335
W--> 681 340      gaa agc tac atc tcc agg cag acc agt gag act gta gaa
W--> 682 aat gac aac      1229Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp
E--> 683 asn      345      350      355      360
W--> 684 gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa      1280Ala Ser
W--> 685 Ser Phe Thr Met
W--> 686 365      gcctttgtga aacttgctat
E--> 687 tacatgtga      1309
```

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<210> 11
<211> 20
<212> DNA
<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat MIP-3 gene transcript.

*do NOT use scientific symbols or foreign accent
marks*

*↓ global
error*

*(They cannot be
processed by CLF
software.)*

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/13/2005
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 47,48,49,50,51,52,53,54,55,56,57,59,60,61
Seq#:3; Line(s) 104,105,107,108,109,110,111,112,113,114,115,116,117,118,119
Seq#:5; Line(s) 161,162,163,164,165,166,167,168,169,170,171,172,173,174,175
Seq#:5; Line(s) 176,177
Seq#:7; Line(s) 211,212,213,214,215,216,217,218,219,220,221,222,223,224,225
Seq#:7; Line(s) 226,227,228,229,230,231,232,233,234,235,236,237,238,239,240
Seq#:7; Line(s) 241,242,243,244,245,246,247,248,249,250,251,252,253,254,255
Seq#:7; Line(s) 256,257,258,259,260,261,262,263,264,265,266,267,268,269,270
Seq#:7; Line(s) 271
Seq#:9; Line(s) 340,341,342,343,344,345,346,347,348,349,350,351,352,353,354
Seq#:9; Line(s) 355,356,357,358,359,360,361,362,363,364,365,366,367,368,369
Seq#:9; Line(s) 370,371,372,373,374,375,376,377,378,379,380,381,382,383,384
Seq#:9; Line(s) 385,386,387,388,389,390,391,392,393,394,395,396,397,398
Seq#:13; Line(s) 496,497,498,499,500,501,502,503,504,505,506,507,508,509
Seq#:13; Line(s) 510,511,512,513,514,515,516,517,518,519,520,521,522,523
Seq#:13; Line(s) 524,525,526,527,528,529,530,531,532,533,534,535,536,537
Seq#:13; Line(s) 538,539,540,541,542,543,544,545,546,547,548,549,550,551
Seq#:13; Line(s) 552,553,554,555,556
Seq#:15; Line(s) 625,626,627,628,629,630,631,632,633,634,635,636,637,638
Seq#:15; Line(s) 639,640,641,642,643,644,645,646,647,648,649,650,651,652
Seq#:15; Line(s) 653,654,655,656,657,658,659,660,661,662,663,664,665,666
Seq#:15; Line(s) 667,668,669,670,671,672,673,674,675,676,677,678,679,680
Seq#:15; Line(s) 681,682,683,684,685

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,16,17,18,19,20,21

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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:34
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:44
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:1
L:48 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:48 M:112 C: (48) String data converted to lower case,
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:25
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:51 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
M:112 Repeated in SeqNo=1
L:52 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
M:341 Repeated in SeqNo=1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:58 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:62 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:127 SEQ:1
L:98 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:91
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:96
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:101
L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:105 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:3
L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:105 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=3
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17

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Output Set: N:\CRF4\09132005\J547532.raw

L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:22
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
M:112 Repeated in SeqNo=3
L:112 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
M:341 Repeated in SeqNo=3
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:116 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:118 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:119 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:106 SEQ:3
L:155 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:148
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:153
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:158
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:162 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:5
L:162 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:162 M:112 C: (48) String data converted to lower case,
L:163 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:164 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:25
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
M:254 Repeated in SeqNo=5
L:165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:112 Repeated in SeqNo=5
L:166 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:167 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
M:341 Repeated in SeqNo=5

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Output Set: N:\CRF4\09132005\J547532.raw

L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:170 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:171 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:172 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:175 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:176 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:177 M:252 E: No. of Seq. differs, <211> LENGTH:Input:291 Found:118 SEQ:5
L:210 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7, Line#:208
L:211 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:7
L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:212 M:112 C: (48) String data converted to lower case,
L:213 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:214 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
M:254 Repeated in SeqNo=7
L:215 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=7
L:216 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:217 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:219 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
M:341 Repeated in SeqNo=7
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:220 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:221 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:222 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:223 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:224 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:226 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

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Output Set: N:\CRF4\09132005\J547532.raw

L:227 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:228 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:229 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:230 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:231 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:232 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:233 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:234 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:241 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:246 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:254 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:259 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:272 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1122 Found:294 SEQ:7
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:337
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:341 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:9
L:341 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:341 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=9
L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
M:112 Repeated in SeqNo=9
M:341 Repeated in SeqNo=9
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:352 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:357 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:362 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:378 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:383 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:388 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:391 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:396 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:399 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1101 Found:294 SEQ:9
L:490 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:488
L:491 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
M:254 Repeated in SeqNo=13
L:496 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:341 Repeated in SeqNo=13
L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:112 Repeated in SeqNo=13
L:499 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:502 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6

VERIFICATION SUMMARY DATE: 09/13/2005
PATENT APPLICATION: US/10/547,532 TIME: 13:24:42

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\09132005\J547532.raw

L:507 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:512 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:517 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:522 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:525 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:530 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:535 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:557 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1502 Found:528 SEQ:13
L:622 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:620
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
M:254 Repeated in SeqNo=15
M:341 Repeated in SeqNo=15
M:112 Repeated in SeqNo=15
L:687 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1309 Found:470 SEQ:15